

**Amendments to the Specification:**

Please replace paragraph [0136] of U.S. Patent Publ. No. 20070269432 with the following amended paragraph:

-- The region [A] hybridizes to [A'], and then a loop consisting of region [B] is formed.

The loop sequence may be preferably 3 to 23 nucleotide in length. The loop sequence, for example, can be selected from group consisting of following sequences ([http://www.ambion.com/techlib/tb/tb\\_506.html](http://www.ambion.com/techlib/tb/tb_506.html)). Furthermore, loop sequence consisting of 23 nucleotides also provides active siRNA (Jacque, J.-M., Triques, K., and Stevenson, M. (2002) Modulation of HIV-1 replication by RNA interference. *Nature* 418: 435-438.).--

Please replace paragraph [0142] with the following amended paragraph:

-- The nucleotide sequence of suitable siRNAs can be designed using an siRNA design computer program available from the Ambion website ([http://www.ambion.com/techlib/misc/siRNA\\_finder.html](http://www.ambion.com/techlib/misc/siRNA_finder.html)). The computer program selects nucleotide sequences for siRNA synthesis based on the following protocol.--

Please replace paragraph [0144] with the following amended paragraph:

-- 2. Compare the potential target sites to the human genome database and eliminate from consideration any target sequences with significant homology to other coding sequences. The homology search can be performed using BLAST, which can be found on the NCBI server at: [www.ncbi.nlm.nih.gov/BLAST/](http://www.ncbi.nlm.nih.gov/BLAST/).

Please replace paragraph [0197] with the following amended paragraph:

An unsupervised hierarchical clustering method was applied to both genes and tumors. To obtain reproducible clusters for classification of the 102 samples, 710 genes for which valid data were obtained in 80% of the experiments, and whose expression ratios varied by standard deviations

of more than 1.1, were selected. The analysis was performed using web-available software ("Cluster" and "Tree View") written by M. Eisen (<http://at.genome-www5.stanford.edu/MicroArray/SMD/restech.html>). Before applying the clustering algorithm, the fluorescence ratio for each spot was log-transformed and then median-centered the data for each sample to remove experimental biases and used average linkage.